

SEQUENCE LISTING

<110> Turner, C. Alexander Jr.
Nehls, Michael
Friedrich, Glenn
Scoville, John
Zambrowicz, Brian
Sands, Arthur T.

<120> Novel Human 7TM Proteins and Receptors and
Polynucleotides Encoding the Same

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<150> US 60/153,366

<151> 1999-09-10

<150> US 60/165,510

<151> 1999-11-15

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<210> 4

<211> 1221

<212> PRT

<213> homo sapiens

<400> 4

Met Phe Arg Ser Asp Arg Met Trp Ser Cys His Trp Lys Trp Lys Pro

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20	25	30	
Ser Ala Val Trp Gly Cys Ala Asn Cys Arg Val Val Leu Ser Asn Pro			
35	40	45	
Ser Gly Thr Phe Thr Ser Pro Cys Tyr Pro Asn Asp Tyr Pro Asn Ser			
50	55	60	
Gln Ala Cys Met Trp Thr Leu Arg Ala Pro Thr Gly Tyr Ile Ile Gln			
65	70	75	80
Ile Thr Phe Asn Asp Phe Asp Ile Glu Glu Ala Pro Asn Cys Ile Tyr			
85	90	95	
Asp Ser Leu Ser Leu Asp Asn Gly Glu Ser Gln Thr Lys Phe Cys Gly			
100	105	110	
Ala Thr Ala Lys Gly Leu Ser Phe Asn Ser Ser Ala Asn Glu Met His			
115	120	125	
Val Ser Phe Ser Ser Asp Phe Ser Ile Gln Lys Lys Gly Phe Asn Ala			
130	135	140	
Ser Tyr Ile Arg Val Ala Val Ser Leu Arg Asn Gln Lys Val Ile Leu			
145	150	155	160
Pro Gln Thr Ser Asp Ala Tyr Gln Val Ser Val Ala Lys Ser Ile Ser			
165	170	175	
Ile Pro Glu Leu Ser Ala Phe Thr Leu Cys Phe Glu Ala Thr Lys Val			
180	185	190	
Gly His Glu Asp Ser Asp Trp Thr Ala Phe Ser Tyr Ser Asn Ala Ser			
195	200	205	
Phe Thr Gln Leu Leu Ser Phe Gly Lys Ala Lys Ser Gly Tyr Phe Leu			
210	215	220	
Ser Ile Ser Asp Ser Lys Cys Leu Leu Asn Asn Ala Leu Pro Val Lys			
225	230	235	240
Glu Lys Glu Asp Ile Phe Ala Glu Ser Phe Glu Gln Leu Cys Leu Val			
245	250	255	
Trp Asn Asn Ser Leu Gly Ser Ile Gly Val Asn Phe Lys Arg Asn Tyr			
260	265	270	
Glu Thr Val Pro Cys Asp Ser Thr Ile Ser Lys Val Ile Pro Gly Asn			
275	280	285	
Gly Lys Leu Leu Leu Gly Ser Asn Gln Asn Glu Ile Val Ser Leu Lys			
290	295	300	
Gly Asp Ile Tyr Asn Phe Arg Leu Trp Asn Phe Thr Met Asn Ala Lys			
305	310	315	320
Ile Leu Ser Asn Leu Ser Cys Asn Val Lys Gly Asn Val Val Asp Trp			
325	330	335	
Gln Asn Asp Phe Trp Asn Ile Pro Asn Leu Ala Leu Lys Ala Glu Ser			
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Asn Leu Ser Cys Gly Ser Tyr Leu Ile Pro Leu Pro Ala Ala Glu Leu			
355	360	365	
Ala Ser Cys Ala Asp Leu Gly Thr Leu Cys Gln Ala Thr Val Asn Ser			
370	375	380	
Pro Ser Thr Thr Pro Pro Thr Val Thr Thr Asn Met Pro Val Thr Asn			
385	390	395	400
Arg Ile Asp Lys Gln Arg Asn Asp Gly Ile Ile Tyr Arg Ile Ser Val			
405	410	415	
Val Ile Gln Asn Ile Leu Arg His Pro Glu Val Lys Val Gln Ser Lys			
420	425	430	
Val Ala Glu Trp Leu Asn Ser Thr Phe Gln Asn Trp Asn Tyr Thr Val			
435	440	445	
Tyr Val Val Asn Ile Ser Phe His Leu Ser Ala Gly Glu Asp Lys Ile			

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Lys Val Lys Arg Ser	Leu Glu Asp Glu Pro Arg	Leu Val Leu Trp Ala		
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Leu Leu Val Tyr Asn	Ala Thr Asn Asn Thr Asn	Leu Glu Gly Lys Ile		
485	490	495		
Ile Gln Gln Lys Leu	Leu Lys Asn Asn Glu Ser	Leu Asp Glu Gly Leu		
500	505	510		
Arg Leu His Thr Val	Asn Val Arg Gln Leu Gly	His Cys Leu Ala Met		
515	520	525		
Glu Glu Pro Lys Gly	Tyr Tyr Trp Pro Ser Ile	Gln Pro Ser Glu Tyr		
530	535	540		
Val Leu Pro Cys Pro	Asp Lys Pro Gly Phe Ser	Ala Ser Arg Ile Cys		
545	550	555	560	
Phe Tyr Asn Ala Thr	Asn Pro Leu Val Thr Tyr	Trp Gly Pro Val Asp		
565	570	575		
Ile Ser Asn Cys Leu	Lys Glu Ala Asn Glu Val	Ala Asn Gln Ile Leu		
580	585	590		
Asn Leu Thr Ala Asp	Gly Gln Asn Leu Thr Ser	Ala Asn Ile Thr Asn		
595	600	605		
Ile Val Glu Gln Val	Lys Arg Ile Val Asn Lys	Glu Glu Asn Ile Asp		
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625	630	635	640	
Ser Ser Asp Ser Asp	Leu Leu Glu Ser Ser	Ser Glu Ala Leu Lys Thr		
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Ile Asp Glu Leu Ala	Phe Lys Ile Asp Leu Asn	Ser Thr Ser His Val		
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Asn Ile Thr Thr Arg	Asn Leu Ala Leu Ser Val	Ser Ser Leu Leu Pro		
675	680	685		
Gly Thr Asn Ala Ile	Ser Asn Phe Ser Ile Gly	Leu Pro Ser Asn Asn		
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Glu Ser Tyr Phe Gln	Met Asp Phe Glu Ser Gly	Gln Val Asp Pro Leu		
705	710	715	720	
Ala Ser Val Ile Leu	Pro Pro Asn Leu Leu Glu	Asn Leu Ser Pro Glu		
725	730	735		
Asp Ser Val Leu Val	Arg Arg Ala Gln Phe Thr	Phe Phe Asn Lys Thr		
740	745	750		
Gly Leu Phe Gln Asp	Val Gly Pro Gln Arg Lys	Thr Leu Val Ser Tyr		
755	760	765		
Val Met Ala Cys Ser	Ile Gly Asn Ile Thr Ile	Gln Asn Leu Lys Asp		
770	775	780		
Pro Val Gln Ile Lys	Ile Lys His Thr Arg Thr	Gln Glu Val His His		
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Pro Ile Cys Ala Phe	Trp Asp Leu Asn Lys Asn	Lys Ser Phe Gly Gly		
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Trp Asn Thr Ser Gly	Cys Val Ala His Arg Asp	Ser Asp Ala Ser Glu		
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Thr Val Cys Leu Cys	Asn His Phe Thr His Phe	Gly Val Leu Met Asp		
835	840	845		
Leu Pro Arg Ser Ala	Ser Gln Leu Asp Ala Arg	Asn Thr Lys Val Leu		
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Thr Phe Ile Ser Tyr	Ile Gly Cys Gly Ile Ser	Ala Ile Phe Ser Ala		
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Ala Thr Leu Leu Thr	Tyr Val Ala Phe Glu Lys	Leu Arg Arg Asp Tyr		
885	890	895		
Pro Ser Lys Ile Leu	Met Asn Leu Ser Thr Ala	Leu Leu Phe Leu Asn		

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Leu Leu Phe Leu Leu Asp Gly Trp Ile Thr Ser Phe Asn Val Asp Gly		
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Leu Cys Ile Ala Val Ala Val Leu Leu His Phe Phe Leu Leu Ala Thr		
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Phe Thr Trp Met Gly Leu Glu Ala Ile His Met Tyr Ile Ala Leu Val		
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Lys Val Phe Asn Thr Tyr Ile Arg Arg Tyr Ile Leu Lys Phe Cys Ile		
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Ile Gly Trp Gly Leu Pro Ala Leu Val Val Ser Val Val Leu Ala Ser		
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Arg Asn Asn Asn Glu Val Tyr Gly Lys Glu Ser Tyr Gly Lys Glu Lys		
995	1000	1005
Gly Asp Glu Phe Cys Trp Ile Gln Asp Pro Val Ile Phe Tyr Val Thr		
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Cys Ala Gly Tyr Phe Gly Val Met Phe Phe Leu Asn Ile Ala Met Phe		
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Ile Val Val Met Val Glu Ile Cys Gly Arg Asn Gly Lys Arg Ser Asn		
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Arg Thr Leu Arg Glu Glu Val Leu Arg Asn Leu Arg Ser Val Val Ser		
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Leu Gln Gly Leu Phe Ile Phe Ile Phe His Cys Ala Met Lys Glu Asn		
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Val Gln Lys Gln Trp Arg Arg His Leu Cys Cys Gly Arg Phe Arg Leu		
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Ala Asp Asn Ser Asp Trp Ser Lys Thr Ala Thr Asn Ile Ile Lys Lys		
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Ser Ser Asp Asn Leu Gly Lys Ser Leu Ser Ser Ser Ser Ile Gly Ser		
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Asn Ser Thr Tyr Leu Thr Ser Lys Ser Lys Ser Ser Ser Thr Thr Tyr		
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Phe Lys Arg Asn Ser His Thr Asp Asn Val Ser Tyr Glu His Ser Phe		
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<211> 2157

<212> DNA

<213> homo sapiens

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<210> 6

<211> 718

<212> PRT

<213> homo sapiens

<400> 6

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			20					25					30		
Ser	Ala	Val	Trp	Gly	Cys	Ala	Asn	Cys	Arg	Val	Val	Leu	Ser	Asn	Pro
			35				40					45			
Ser	Gly	Thr	Phe	Thr	Ser	Pro	Cys	Tyr	Pro	Asn	Asp	Tyr	Pro	Asn	Ser
	50					55					60				
Gln	Ala	Cys	Met	Trp	Thr	Leu	Arg	Ala	Pro	Thr	Gly	Tyr	Ile	Ile	Gln
65						70				75				80	
Ile	Thr	Phe	Asn	Asp	Phe	Asp	Ile	Glu	Glu	Ala	Pro	Asn	Cys	Ile	Tyr
				85					90					95	
Asp	Ser	Leu	Ser	Leu	Asp	Asn	Gly	Glu	Ser	Gln	Thr	Lys	Phe	Cys	Gly
			100				105						110		
Ala	Thr	Ala	Lys	Gly	Leu	Ser	Phe	Asn	Ser	Ser	Ala	Asn	Glu	Met	His
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Val	Ser	Phe	Ser	Ser	Asp	Phe	Ser	Ile	Gln	Lys	Lys	Gly	Phe	Asn	Ala
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Ser	Tyr	Ile	Arg	Val	Ala	Val	Ser	Leu	Arg	Asn	Gln	Lys	Val	Ile	Leu
145					150					155				160	
Pro	Gln	Thr	Ser	Asp	Ala	Tyr	Gln	Val	Ser	Val	Ala	Lys	Ser	Ile	Ser

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			180					185					190		
Gly	His	Glu	Asp	Ser	Asp	Trp	Thr	Ala	Phe	Ser	Tyr	Ser	Asn	Ala	Ser
		195					200					205			
Phe	Thr	Gln	Leu	Leu	Ser	Phe	Gly	Lys	Ala	Lys	Ser	Gly	Tyr	Phe	Leu
	210					215					220				
Ser	Ile	Ser	Asp	Ser	Lys	Cys	Leu	Leu	Asn	Asn	Ala	Leu	Pro	Val	Lys
225					230					235					240
Glu	Lys	Glu	Asp	Ile	Phe	Ala	Glu	Ser	Phe	Glu	Gln	Leu	Cys	Leu	Val
			245						250					255	
Trp	Asn	Asn	Ser	Leu	Gly	Ser	Ile	Gly	Val	Asn	Phe	Lys	Arg	Asn	Tyr
			260					265					270		
Glu	Thr	Val	Pro	Cys	Asp	Ser	Thr	Ile	Ser	Lys	Val	Ile	Pro	Gly	Asn
		275					280					285			
Gly	Lys	Leu	Leu	Leu	Gly	Ser	Asn	Gln	Asn	Glu	Ile	Val	Ser	Leu	Lys
	290					295					300				
Gly	Asp	Ile	Tyr	Asn	Phe	Arg	Leu	Trp	Asn	Phe	Thr	Met	Asn	Ala	Lys
305					310					315					320
Ile	Leu	Ser	Asn	Leu	Ser	Cys	Asn	Val	Lys	Gly	Asn	Val	Val	Asp	Trp
			325						330					335	
Gln	Asn	Asp	Phe	Trp	Asn	Ile	Pro	Asn	Leu	Ala	Leu	Lys	Ala	Glu	Ser
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Asn	Leu	Ser	Cys	Gly	Ser	Tyr	Leu	Ile	Pro	Leu	Pro	Ala	Ala	Glu	Leu
		355					360					365			
Ala	Ser	Cys	Ala	Asp	Leu	Gly	Thr	Leu	Cys	Gln	Ala	Thr	Val	Asn	Ser
	370					375					380				
Pro	Ser	Thr	Thr	Pro	Pro	Thr	Val	Thr	Thr	Asn	Met	Pro	Val	Thr	Asn
385					390					395					400
Arg	Ile	Asp	Lys	Gln	Arg	Asn	Asp	Gly	Ile	Ile	Tyr	Arg	Ile	Ser	Val
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Val	Ile	Gln	Asn	Ile	Leu	Arg	His	Pro	Glu	Val	Lys	Val	Gln	Ser	Lys
			420					425					430		
Val	Ala	Glu	Trp	Leu	Asn	Ser	Thr	Phe	Gln	Asn	Trp	Asn	Tyr	Thr	Val
		435					440					445			
Tyr	Val	Val	Asn	Ile	Ser	Phe	His	Leu	Ser	Ala	Gly	Glu	Asp	Lys	Ile
	450					455					460				
Lys	Val	Lys	Arg	Ser	Leu	Glu	Asp	Glu	Pro	Arg	Leu	Val	Leu	Trp	Ala
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Leu	Leu	Val	Tyr	Asn	Ala	Thr	Asn	Asn	Thr	Asn	Leu	Glu	Gly	Lys	Ile
			485						490					495	
Ile	Gln	Gln	Lys	Leu	Leu	Lys	Asn	Asn	Glu	Ser	Leu	Asp	Glu	Gly	Leu
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Arg	Leu	His	Thr	Val	Asn	Val	Arg	Gln	Leu	Gly	His	Cys	Leu	Ala	Met
		515					520					525			
Glu	Glu	Pro	Lys	Gly	Tyr	Tyr	Trp	Pro	Ser	Ile	Gln	Pro	Ser	Glu	Tyr
	530					535					540				
Val	Leu	Pro	Cys	Pro	Asp	Lys	Pro	Gly	Phe	Ser	Ala	Ser	Arg	Ile	Cys
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Phe	Tyr	Asn	Ala	Thr	Asn	Pro	Leu	Val	Thr	Tyr	Trp	Gly	Pro	Val	Asp
			565						570					575	
Ile	Ser	Asn	Cys	Leu	Lys	Glu	Ala	Asn	Glu	Val	Ala	Asn	Gln	Ile	Leu
			580					585					590		
Asn	Leu	Thr	Ala	Asp	Gly	Gln	Asn	Leu	Thr	Ser	Ala	Asn	Ile	Thr	Asn
		595					600					605			
Ile	Val	Glu	Gln	Val	Lys	Arg	Ile	Val	Asn	Lys	Glu	Glu	Asn	Ile	Asp

610		615		620
Ile Thr Leu Gly Ser	Thr Leu Met Asn Ile Phe	Ser Asn Ile Leu Ser		
625	630	635	640	
Ser Ser Asp Ser Asp	Leu Leu Glu Ser Ser Ser	Glu Ala Leu Lys Thr		
	645	650	655	
Ile Asp Glu Leu Ala Phe Lys Ile	Asp Leu Asn Ser Thr Ser His Val			
	660	665	670	
Asn Ile Thr Thr Arg Asn Leu Ala Leu Ser Val	Ser Ser Leu Leu Pro			
	675	680	685	
Gly Thr Asn Ala Ile Ser Asn Phe Ser Ile Gly	Leu Pro Ser Asn Asn			
	690	695	700	
Glu Ser Tyr Phe Gln Val Met Ser Gln Trp Phe	Leu Ser Phe			
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 <212> DNA
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<400> 7

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<212> PRT

<213> homo sapiens

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<210> 16

<211> 1111

<212> PRT

<213> homo sapiens

<400> 16

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Ser	Pro	Leu	Leu	Phe	Leu	Phe	Ala	Leu	Tyr	Ile	Met	Cys	Val	Pro	His
		20					25						30		
Ser	Val	Trp	Gly	Cys	Ala	Asn	Cys	Arg	Val	Val	Leu	Ser	Asn	Pro	Ser
	35						40					45			
Gly	Thr	Phe	Thr	Ser	Pro	Cys	Tyr	Pro	Asn	Asp	Tyr	Pro	Asn	Ser	Gln
50						55					60				
Ala	Cys	Met	Trp	Thr	Leu	Arg	Ala	Pro	Thr	Gly	Tyr	Ile	Ile	Gln	Ile
65					70					75					80
Thr	Phe	Asn	Asp	Phe	Asp	Ile	Glu	Glu	Ala	Pro	Asn	Cys	Ile	Tyr	Asp
			85						90					95	
Ser	Leu	Ser	Leu	Asp	Asn	Gly	Glu	Ser	Gln	Thr	Lys	Phe	Cys	Gly	Ala
			100					105					110		
Thr	Ala	Lys	Gly	Leu	Ser	Phe	Asn	Ser	Ser	Ala	Asn	Glu	Met	His	Val
		115					120					125			
Ser	Phe	Ser	Ser	Asp	Phe	Ser	Ile	Gln	Lys	Lys	Gly	Phe	Asn	Ala	Ser
	130					135					140				
Tyr	Ile	Arg	Val	Ala	Val	Ser	Leu	Arg	Asn	Gln	Lys	Val	Ile	Leu	Pro
145					150					155					160
Gln	Thr	Ser	Asp	Ala	Tyr	Gln	Val	Ser	Val	Ala	Lys	Ser	Ile	Ser	Ile
			165						170					175	
Pro	Glu	Leu	Ser	Ala	Phe	Thr	Leu	Cys	Phe	Glu	Ala	Thr	Lys	Val	Gly
			180					185					190		
His	Glu	Asp	Ser	Asp	Trp	Thr	Ala	Phe	Ser	Tyr	Ser	Asn	Ala	Ser	Phe
		195					200					205			
Thr	Gln	Leu	Leu	Ser	Phe	Gly	Lys	Ala	Lys	Ser	Gly	Tyr	Phe	Leu	Ser
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Ile	Ser	Asp	Ser	Lys	Cys	Leu	Leu	Asn	Asn	Ala	Leu	Pro	Val	Lys	Glu
225					230					235					240
Lys	Glu	Asp	Ile	Phe	Ala	Glu	Ser	Phe	Glu	Gln	Leu	Cys	Leu	Val	Trp
				245					250					255	
Asn	Asn	Ser	Leu	Gly	Ser	Ile	Gly	Val	Asn	Phe	Lys	Arg	Asn	Tyr	Glu
			260					265					270		
Thr	Val	Pro	Cys	Asp	Ser	Thr	Ile	Ser	Lys	Val	Ile	Pro	Gly	Asn	Gly
		275					280					285			
Lys	Leu	Leu	Leu	Gly	Ser	Asn	Gln	Asn	Glu	Ile	Val	Ser	Leu	Lys	Gly
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Asp	Ile	Tyr	Asn	Phe	Arg	Leu	Trp	Asn	Phe	Thr	Met	Asn	Ala	Lys	Ile
305					310					315					320
Leu	Ser	Asn	Leu	Ser	Cys	Asn	Val	Lys	Gly	Asn	Val	Val	Asp	Trp	Gln
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Asn	Asp	Phe	Trp	Asn	Ile	Pro	Asn	Leu	Ala	Leu	Lys	Ala	Glu	Ser	Asn
			340					345					350		
Leu	Ser	Cys	Gly	Ser	Tyr	Leu	Ile	Pro	Leu	Pro	Ala	Ala	Glu	Leu	Ala
		355					360					365			
Ser	Cys	Ala	Asp	Leu	Gly	Thr	Leu	Cys	Gln	Ala	Thr	Val	Asn	Ser	Pro
	370					375					380				
Ser	Thr	Thr	Pro	Pro	Thr	Val	Thr	Thr	Asn	Met	Pro	Val	Thr	Asn	Arg
385					390					395					400
Ile	Asp	Lys	Gln	Arg	Asn	Asp	Gly	Ile	Ile	Tyr	Arg	Ile	Ser	Val	Val
			405						410					415	
Ile	Gln	Asn	Ile	Leu	Arg	His	Pro	Glu	Val	Lys	Val	Gln	Ser	Lys	Val
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Ala	Glu	Trp	Leu	Asn	Ser	Thr	Phe	Gln	Asn	Trp	Asn	Tyr	Thr	Val	Tyr

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Val Val Asn Ile Ser Phe His Leu Ser Ala Gly Glu Asp Lys Ile Lys		
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Val Lys Arg Ser Leu Glu Asp Glu Pro Arg Leu Val Leu Trp Ala Leu		
465	470	475
Leu Val Tyr Asn Ala Thr Asn Asn Thr Asn Leu Glu Gly Lys Ile Ile		
485	490	495
Gln Gln Lys Leu Lys Asn Asn Glu Ser Leu Asp Glu Gly Leu Arg		
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Leu His Thr Val Asn Val Arg Gln Leu Gly His Cys Leu Ala Met Glu		
515	520	525
Glu Pro Lys Gly Tyr Tyr Trp Pro Ser Ile Gln Pro Ser Glu Tyr Val		
530	535	540
Leu Pro Cys Pro Asp Lys Pro Gly Phe Ser Ala Ser Arg Ile Cys Phe		
545	550	555
Tyr Asn Ala Thr Asn Pro Leu Val Thr Tyr Trp Gly Pro Val Asp Ile		
565	570	575
Ser Asn Cys Leu Lys Glu Ala Asn Glu Val Ala Asn Gln Ile Leu Asn		
580	585	590
Leu Thr Ala Asp Gly Gln Asn Leu Thr Ser Ala Asn Ile Thr Asn Ile		
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Val Glu Gln Val Lys Arg Ile Val Asn Lys Glu Glu Asn Ile Asp Ile		
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Thr Leu Gly Ser Thr Leu Met Asn Ile Phe Ser Asn Ile Leu Ser Ser		
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Ser Asp Ser Asp Leu Leu Glu Ser Ser Ser Glu Ala Leu Lys Thr Ile		
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Asp Glu Leu Ala Phe Lys Ile Asp Leu Asn Ser Thr Ser His Val Asn		
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Ile Thr Thr Arg Asn Leu Ala Leu Ser Val Ser Ser Leu Leu Pro Gly		
675	680	685
Thr Asn Ala Ile Ser Asn Phe Ser Ile Gly Leu Pro Ser Asn Asn Glu		
690	695	700
Ser Tyr Phe Gln Met Asp Phe Glu Ser Gly Gln Val Asp Pro Leu Ala		
705	710	715
Ser Val Ile Leu Pro Pro Asn Leu Leu Glu Asn Leu Ser Pro Glu Asp		
725	730	735
Ser Val Leu Val Arg Arg Ala Gln Phe Thr Phe Phe Asn Lys Thr Gly		
740	745	750
Leu Phe Gln Asp Val Gly Pro Gln Arg Lys Thr Leu Val Ser Tyr Val		
755	760	765
Met Ala Cys Ser Ile Gly Asn Ile Thr Ile Gln Asn Leu Lys Asp Pro		
770	775	780
Val Gln Ile Lys Ile Lys His Thr Arg Thr Gln Glu Val His His Pro		
785	790	795
Ile Cys Ala Phe Trp Asp Leu Asn Lys Asn Lys Ser Phe Gly Gly Trp		
805	810	815
Asn Thr Ser Gly Cys Val Ala His Arg Asp Ser Asp Ala Ser Glu Thr		
820	825	830
Val Cys Leu Cys Asn His Phe Thr His Phe Gly Val Leu Met Asp Leu		
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Pro Arg Ser Ala Ser Gln Leu Asp Ala Arg Asn Thr Lys Val Leu Thr		
850	855	860
Phe Ile Ser Tyr Ile Gly Cys Gly Ile Ser Ala Ile Phe Ser Ala Ala		
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Thr Leu Leu Thr Tyr Val Ala Phe Glu Lys Leu Arg Arg Asp Tyr Pro		

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<210> 18

<211> 1250

<212> PRT

<213> homo sapiens

<400> 18

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			20				25					30			
His	Ser	Val	Trp	Gly	Cys	Ala	Asn	Cys	Arg	Val	Val	Leu	Ser	Asn	Pro
		35					40					45			

Ser	Gly	Thr	Phe	Thr	Ser	Pro	Cys	Tyr	Pro	Asn	Asp	Tyr	Pro	Asn	Ser	50	55	60
Gln	Ala	Cys	Met	Trp	Thr	Leu	Arg	Ala	Pro	Thr	Gly	Tyr	Ile	Ile	Gln	65	70	75
Ile	Thr	Phe	Asn	Asp	Phe	Asp	Ile	Glu	Glu	Ala	Pro	Asn	Cys	Ile	Tyr	85	90	95
Asp	Ser	Leu	Ser	Leu	Asp	Asn	Gly	Glu	Ser	Gln	Thr	Lys	Phe	Cys	Gly	100	105	110
Ala	Thr	Ala	Lys	Gly	Leu	Ser	Phe	Asn	Ser	Ser	Ala	Asn	Glu	Met	His	115	120	125
Val	Ser	Phe	Ser	Ser	Asp	Phe	Ser	Ile	Gln	Lys	Lys	Gly	Phe	Asn	Ala	130	135	140
Ser	Tyr	Ile	Arg	Val	Ala	Val	Ser	Leu	Arg	Asn	Gln	Lys	Val	Ile	Leu	145	150	155
Pro	Gln	Thr	Ser	Asp	Ala	Tyr	Gln	Val	Ser	Val	Ala	Lys	Ser	Ile	Ser	165	170	175
Ile	Pro	Glu	Leu	Ser	Ala	Phe	Thr	Leu	Cys	Phe	Glu	Ala	Thr	Lys	Val	180	185	190
Gly	His	Glu	Asp	Ser	Asp	Trp	Thr	Ala	Phe	Ser	Tyr	Ser	Asn	Ala	Ser	195	200	205
Phe	Thr	Gln	Leu	Leu	Ser	Phe	Gly	Lys	Ala	Lys	Ser	Gly	Tyr	Phe	Leu	210	215	220
Ser	Ile	Ser	Asp	Ser	Lys	Cys	Leu	Leu	Asn	Asn	Ala	Leu	Pro	Val	Lys	225	230	235
Glu	Lys	Glu	Asp	Ile	Phe	Ala	Glu	Ser	Phe	Glu	Gln	Leu	Cys	Leu	Val	245	250	255
Trp	Asn	Asn	Ser	Leu	Gly	Ser	Ile	Gly	Val	Asn	Phe	Lys	Arg	Asn	Tyr	260	265	270
Glu	Thr	Val	Pro	Cys	Asp	Ser	Thr	Ile	Ser	Lys	Val	Ile	Pro	Gly	Asn	275	280	285
Gly	Lys	Leu	Leu	Leu	Gly	Ser	Asn	Gln	Asn	Glu	Ile	Val	Ser	Leu	Lys	290	295	300
Gly	Asp	Ile	Tyr	Asn	Phe	Arg	Leu	Trp	Asn	Phe	Thr	Met	Asn	Ala	Lys	305	310	315
Ile	Leu	Ser	Asn	Leu	Ser	Cys	Asn	Val	Lys	Gly	Asn	Val	Val	Asp	Trp	325	330	335
Gln	Asn	Asp	Phe	Trp	Asn	Ile	Pro	Asn	Leu	Ala	Leu	Lys	Ala	Glu	Ser	340	345	350
Asn	Leu	Ser	Cys	Gly	Ser	Tyr	Leu	Ile	Pro	Leu	Pro	Ala	Ala	Glu	Leu	355	360	365
Ala	Ser	Cys	Ala	Asp	Leu	Gly	Thr	Leu	Cys	Gln	Ala	Thr	Val	Asn	Ser	370	375	380
Pro	Ser	Thr	Thr	Pro	Pro	Thr	Val	Thr	Thr	Asn	Met	Pro	Val	Thr	Asn	385	390	395
Arg	Ile	Asp	Lys	Gln	Arg	Asn	Asp	Gly	Ile	Ile	Tyr	Arg	Ile	Ser	Val	405	410	415
Val	Ile	Gln	Asn	Ile	Leu	Arg	His	Pro	Glu	Val	Lys	Val	Gln	Ser	Lys	420	425	430
Val	Ala	Glu	Trp	Leu	Asn	Ser	Thr	Phe	Gln	Asn	Trp	Asn	Tyr	Thr	Val	435	440	445
Tyr	Val	Val	Asn	Ile	Ser	Phe	His	Leu	Ser	Ala	Gly	Glu	Asp	Lys	Ile	450	455	460
Lys	Val	Lys	Arg	Ser	Leu	Glu	Asp	Glu	Pro	Arg	Leu	Val	Leu	Trp	Ala	465	470	475
Leu	Leu	Val	Tyr	Asn	Ala	Thr	Asn	Asn	Thr	Asn	Leu	Glu	Gly	Lys	Ile	485	490	495

Phe Thr Trp Met Gly Leu Glu Ala Ile His Met Tyr Ile Ala Leu Val
 945 950 955 960
 Lys Val Phe Asn Thr Tyr Ile Arg Arg Tyr Ile Leu Lys Phe Cys Ile
 965 970 975
 Ile Gly Trp Gly Leu Pro Ala Leu Val Val Ser Val Val Leu Ala Ser
 980 985 990
 Arg Asn Asn Asn Glu Val Tyr Gly Lys Glu Ser Tyr Gly Lys Glu Lys
 995 1000 1005
 Gly Asp Glu Phe Cys Trp Ile Gln Asp Pro Val Ile Phe Tyr Val Thr
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 Cys Ala Gly Tyr Phe Gly Val Met Phe Phe Leu Asn Ile Ala Met Phe
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 Ile Val Val Met Val Gln Ile Cys Gly Arg Asn Gly Lys Arg Ser Asn
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<210> 22

<211> 718

<212> PRT

<213> homo sapiens

<400> 22

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Gln Ala Cys Met Trp Thr Leu Arg Ala Pro Thr Gly Tyr Ile Ile Gln	
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Asp Ser Leu Ser Leu Asp Asn Gly Glu Ser Gln Thr Lys Phe Cys Gly	
100 105 110	
Ala Thr Ala Lys Gly Leu Ser Phe Asn Ser Ser Ala Asn Glu Met His	
115 120 125	

Val	Ser	Phe	Ser	Ser	Asp	Phe	Ser	Ile	Gln	Lys	Lys	Gly	Phe	Asn	Ala
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Ser	Tyr	Ile	Arg	Val	Ala	Val	Ser	Leu	Arg	Asn	Gln	Lys	Val	Ile	Leu
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Pro	Gln	Thr	Ser	Asp	Ala	Tyr	Gln	Val	Ser	Val	Ala	Lys	Ser	Ile	Ser
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Ile	Pro	Glu	Leu	Ser	Ala	Phe	Thr	Leu	Cys	Phe	Glu	Ala	Thr	Lys	Val
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Gly	His	Glu	Asp	Ser	Asp	Trp	Thr	Ala	Phe	Ser	Tyr	Ser	Asn	Ala	Ser
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Phe	Thr	Gln	Leu	Leu	Ser	Phe	Gly	Lys	Ala	Lys	Ser	Gly	Tyr	Phe	Leu
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Ser	Ile	Ser	Asp	Ser	Lys	Cys	Leu	Leu	Asn	Asn	Ala	Leu	Pro	Val	Lys
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Gln	Asn	Asp	Phe	Trp	Asn	Ile	Pro	Asn	Leu	Ala	Leu	Lys	Ala	Glu	Ser
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Lys	Val	Lys	Arg	Ser	Leu	Glu	Asp	Glu	Pro	Arg	Leu	Val	Leu	Trp	Ala
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Ile	Gln	Gln	Lys	Leu	Leu	Lys	Asn	Asn	Glu	Ser	Leu	Asp	Glu	Gly	Leu
			500					505					510		
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	515						520					525			
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Phe	Tyr	Asn	Ala	Thr	Asn	Pro	Leu	Val	Thr	Tyr	Trp	Gly	Pro	Val	Asp
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 Asn Leu Thr Ala Asp Gly Gln Asn Leu Thr Ser Ala Asn Ile Thr Asn
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 Ile Val Glu Gln Val Lys Arg Ile Val Asn Lys Glu Glu Asn Ile Asp
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 Ile Thr Leu Gly Ser Thr Leu Met Asn Ile Phe Ser Asn Ile Leu Ser
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 Ser Ser Asp Ser Asp Leu Leu Glu Ser Ser Ser Glu Ala Leu Lys Thr
 645 650 655
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<210> 23

<211> 3339

<212> DNA

<213> homo sapiens

<400> 23

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<211> 1112

<212> PRT

<213> homo sapiens

<400> 24

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			20					25					30		
His	Ser	Val	Trp	Gly	Cys	Ala	Asn	Cys	Arg	Val	Val	Leu	Ser	Asn	Pro
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Ser	Gly	Thr	Phe	Thr	Ser	Pro	Cys	Tyr	Pro	Asn	Asp	Tyr	Pro	Asn	Ser
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Asp	Ser	Leu	Ser	Leu	Asp	Asn	Gly	Glu	Ser	Gln	Thr	Lys	Phe	Cys	Gly
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Ala	Thr	Ala	Lys	Gly	Leu	Ser	Phe	Asn	Ser	Ser	Ala	Asn	Glu	Met	His
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Val	Ser	Phe	Ser	Ser	Asp	Phe	Ser	Ile	Gln	Lys	Lys	Gly	Phe	Asn	Ala
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Ser	Tyr	Ile	Arg	Val	Ala	Val	Ser	Leu	Arg	Asn	Gln	Lys	Val	Ile	Leu
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Pro	Gln	Thr	Ser	Asp	Ala	Tyr	Gln	Val	Ser	Val	Ala	Lys	Ser	Ile	Ser
			165					170					175		
Ile	Pro	Glu	Leu	Ser	Ala	Phe	Thr	Leu	Cys	Phe	Glu	Ala	Thr	Lys	Val
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Gly	His	Glu	Asp	Ser	Asp	Trp	Thr	Ala	Phe	Ser	Tyr	Ser	Asn	Ala	Ser
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Phe	Thr	Gln	Leu	Leu	Ser	Phe	Gly	Lys	Ala	Lys	Ser	Gly	Tyr	Phe	Leu
	210					215					220				
Ser	Ile	Ser	Asp	Ser	Lys	Cys	Leu	Leu	Asn	Asn	Ala	Leu	Pro	Val	Lys
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Glu	Lys	Glu	Asp	Ile	Phe	Ala	Glu	Ser	Phe	Glu	Gln	Leu	Cys	Leu	Val
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Trp	Asn	Asn	Ser	Leu	Gly	Ser	Ile	Gly	Val	Asn	Phe	Lys	Arg	Asn	Tyr
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Glu	Thr	Val	Pro	Cys	Asp	Ser	Thr	Ile	Ser	Lys	Val	Ile	Pro	Gly	Asn
		275					280					285			
Gly	Lys	Leu	Leu	Leu	Gly	Ser	Asn	Gln	Asn	Glu	Ile	Val	Ser	Leu	Lys
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Ile	Leu	Ser	Asn	Leu	Ser	Cys	Asn	Val	Lys	Gly	Asn	Val	Val	Asp	Trp
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Gln	Asn	Asp	Phe	Trp	Asn	Ile	Pro	Asn	Leu	Ala	Leu	Lys	Ala	Glu	Ser
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Asn	Leu	Ser	Cys	Gly	Ser	Tyr	Leu	Ile	Pro	Leu	Pro	Ala	Ala	Glu	Leu
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Ala	Ser	Cys	Ala	Asp	Leu	Gly	Thr	Leu	Cys	Gln	Ala	Thr	Val	Asn	Ser
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Pro	Ser	Thr	Thr	Pro	Pro	Thr	Val	Thr	Thr	Asn	Met	Pro	Val	Thr	Asn
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Arg	Ile	Asp	Lys	Gln	Arg	Asn	Asp	Gly	Ile	Ile	Tyr	Arg	Ile	Ser	Val
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			420					425					430		
Val	Ala	Glu	Trp	Leu	Asn	Ser	Thr	Phe	Gln	Asn	Trp	Asn	Tyr	Thr	Val
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Tyr	Val	Val	Asn	Ile	Ser	Phe	His	Leu	Ser	Ala	Gly	Glu	Asp	Lys	Ile
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Leu	Leu	Val	Tyr	Asn	Ala	Thr	Asn	Asn	Thr	Asn	Leu	Glu	Gly	Lys	Ile
				485					490					495	
Ile	Gln	Gln	Lys	Leu	Leu	Lys	Asn	Asn	Glu	Ser	Leu	Asp	Glu	Gly	Leu
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Arg	Leu	His	Thr	Val	Asn	Val	Arg	Gln	Leu	Gly	His	Cys	Leu	Ala	Met
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Glu	Glu	Pro	Lys	Gly	Tyr	Tyr	Trp	Pro	Ser	Ile	Gln	Pro	Ser	Glu	Tyr
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Val	Leu	Pro	Cys	Pro	Asp	Lys	Pro	Gly	Phe	Ser	Ala	Ser	Arg	Ile	Cys
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Phe	Tyr	Asn	Ala	Thr	Asn	Pro	Leu	Val	Thr	Tyr	Trp	Gly	Pro	Val	Asp
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Ile	Ser	Asn	Cys	Leu	Lys	Glu	Ala	Asn	Glu	Val	Ala	Asn	Gln	Ile	Leu
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Asn	Leu	Thr	Ala	Asp	Gly	Gln	Asn	Leu	Thr	Ser	Ala	Asn	Ile	Thr	Asn
	595						600					605			
Ile	Val	Glu	Gln	Val	Lys	Arg	Ile	Val	Asn	Lys	Glu	Glu	Asn	Ile	Asp
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625					630					635					640

Ser	Ser	Asp	Ser	Asp	Leu	Leu	Glu	Ser	Ser	Ser	Glu	Ala	Leu	Lys	Thr
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Ile	Asp	Glu	Leu	Ala	Phe	Lys	Ile	Asp	Leu	Asn	Ser	Thr	Ser	His	Val
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Asn	Ile	Thr	Thr	Arg	Asn	Leu	Ala	Leu	Ser	Val	Ser	Ser	Leu	Leu	Pro
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	690					695					700				
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Ala	Ser	Val	Ile	Leu	Pro	Pro	Asn	Leu	Leu	Glu	Asn	Leu	Ser	Pro	Glu
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Asp	Ser	Val	Leu	Val	Arg	Arg	Ala	Gln	Phe	Thr	Phe	Phe	Asn	Lys	Thr
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Gly	Leu	Phe	Gln	Asp	Val	Gly	Pro	Gln	Arg	Lys	Thr	Leu	Val	Ser	Tyr
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Val	Met	Ala	Cys	Ser	Ile	Gly	Asn	Ile	Thr	Ile	Gln	Asn	Leu	Lys	Asp
	770					775					780				
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785					790					795					800
Pro	Ile	Cys	Ala	Phe	Trp	Asp	Leu	Asn	Lys	Asn	Lys	Ser	Phe	Gly	Gly
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Trp	Asn	Thr	Ser	Gly	Cys	Val	Ala	His	Arg	Asp	Ser	Asp	Ala	Ser	Glu
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Thr	Val	Cys	Leu	Cys	Asn	His	Phe	Thr	His	Phe	Gly	Val	Leu	Met	Asp
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 Val Gly Pro Gln Arg Lys Thr Leu Val Ser Tyr Val Met Ala Cys Ser
 50 55 60
 Ile Gly Asn Ile Thr Ile Gln Asn Leu Lys Asp Pro Val Gln Ile Lys
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Cys	Val	Ala	His	Arg	Asp	Ser	Asp	Ala	Ser	Glu	Thr	Val	Cys	Leu	Cys		
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Asn	His	Phe	Thr	His	Phe	Gly	Val	Leu	Met	Asp	Leu	Pro	Arg	Ser	Ala		
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Ser	Gln	Leu	Asp	Ala	Arg	Asn	Thr	Lys	Val	Leu	Thr	Phe	Ile	Ser	Tyr		
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Ile	Gly	Cys	Gly	Ile	Ser	Ala	Ile	Phe	Ser	Ala	Ala	Thr	Leu	Leu	Thr		
				165					170						175		
Tyr	Val	Ala	Phe	Glu	Lys	Leu	Arg	Arg	Asp	Tyr	Pro	Ser	Lys	Ile	Leu		
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Tyr	Ile	Arg	Arg	Tyr	Ile	Leu	Lys	Phe	Cys	Ile	Ile	Gly	Trp	Gly	Leu		
		260						265					270				
Pro	Ala	Leu	Val	Val	Ser	Val	Val	Leu	Ala	Ser	Arg	Asn	Asn	Asn	Glu		
		275					280					285					
Val	Tyr	Gly	Lys	Glu	Ser	Tyr	Gly	Lys	Glu	Lys	Gly	Asp	Glu	Phe	Cys		
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Gln	Ile	Cys	Gly	Arg	Asn	Gly	Lys	Arg	Ser	Asn	Arg	Thr	Leu	Arg	Glu		
			340					345					350				
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	355						360					365					
Gly	Met	Thr	Trp	Gly	Phe	Ala	Phe	Phe	Ala	Trp	Gly	Pro	Leu	Asn	Ile		
	370					375					380						
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385					390					395					400		
Ile	Phe	Ile	Phe	His	Cys	Ala	Met	Lys	Glu	Asn	Val	Gln	Lys	Gln	Trp		
				405					410					415			
Arg	Arg	His	Leu	Cys	Cys	Gly	Arg	Phe	Arg	Leu	Ala	Asp	Asn	Ser	Asp		
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Gly	Lys	Ser	Leu	Ser	Ser	Ser	Ser	Ile	Gly	Ser	Asn	Ser	Thr	Tyr	Leu		
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Ala	Asp	Gly	Asp	Gln	Thr	Ser	Ile	Ile	Pro	Val	His	Gln	Val	Ile	Asp		
			500					505				510					
Lys	Val	Lys	Gly	Tyr	Cys	Asn	Ala	His	Ser	Asp	Asn	Phe	Tyr	Lys	Asn		
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 35 40 45
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 50 55 60
 Ile Gly Asn Ile Thr Ile Gln Asn Leu Lys Asp Pro Val Gln Ile Lys
 65 70 75 80
 Ile Lys His Thr Arg Thr Gln Glu Val His His Pro Ile Cys Ala Phe
 85 90 95
 Trp Asp Leu Asn Lys Asn Lys Ser Phe Gly Gly Trp Asn Thr Ser Gly
 100 105 110

Cys	Val	Ala	His	Arg	Asp	Ser	Asp	Ala	Ser	Glu	Thr	Val	Cys	Leu	Cys	115	120	125
Asn	His	Phe	Thr	His	Phe	Gly	Val	Leu	Met	Asp	Leu	Pro	Arg	Ser	Ala	130	135	140
Ser	Gln	Leu	Asp	Ala	Arg	Asn	Thr	Lys	Val	Leu	Thr	Phe	Ile	Ser	Tyr	145	150	155
Ile	Gly	Cys	Gly	Ile	Ser	Ala	Ile	Phe	Ser	Ala	Ala	Thr	Leu	Leu	Thr	165	170	175
Tyr	Val	Ala	Phe	Glu	Lys	Leu	Arg	Arg	Asp	Tyr	Pro	Ser	Lys	Ile	Leu	180	185	190
Met	Asn	Leu	Ser	Thr	Ala	Leu	Leu	Phe	Leu	Asn	Leu	Leu	Phe	Leu	Leu	195	200	205
Asp	Gly	Trp	Ile	Thr	Ser	Phe	Asn	Val	Asp	Gly	Leu	Cys	Ile	Ala	Val	210	215	220
Ala	Val	Leu	Leu	His	Phe	Phe	Leu	Leu	Ala	Thr	Phe	Thr	Trp	Met	Gly	225	230	235
Leu	Glu	Ala	Ile	His	Met	Tyr	Ile	Ala	Leu	Val	Lys	Val	Phe	Asn	Thr	245	250	255
Tyr	Ile	Arg	Arg	Tyr	Ile	Leu	Lys	Phe	Cys	Ile	Ile	Gly	Trp	Gly	Leu	260	265	270
Pro	Ala	Leu	Val	Val	Ser	Val	Val	Leu	Ala	Ser	Arg	Asn	Asn	Asn	Glu	275	280	285
Val	Tyr	Gly	Lys	Glu	Ser	Tyr	Gly	Lys	Glu	Lys	Gly	Asp	Glu	Phe	Cys	290	295	300
Trp	Ile	Gln	Asp	Pro	Val	Ile	Phe	Tyr	Val	Thr	Cys	Ala	Gly	Tyr	Phe	305	310	315
Gly	Val	Met	Phe	Phe	Leu	Asn	Ile	Ala	Met	Phe	Ile	Val	Val	Met	Val	325	330	335
Gln	Ile	Cys	Gly	Arg	Asn	Gly	Lys	Arg	Ser	Asn	Arg	Thr	Leu	Arg	Glu	340	345	350
Glu	Val	Leu	Arg	Asn	Leu	Arg	Ser	Val	Val	Ser	Leu	Thr	Phe	Leu	Leu	355	360	365
Gly	Met	Thr	Trp	Gly	Phe	Ala	Phe	Phe	Ala	Trp	Gly	Pro	Leu	Asn	Ile	370	375	380
Pro	Phe	Met	Tyr	Leu	Phe	Ser	Ile	Phe	Asn	Ser	Leu	Gln	Gly	Leu	Phe	385	390	395
Ile	Phe	Ile	Phe	His	Cys	Ala	Met	Lys	Glu	Asn	Val	Gln	Lys	Gln	Trp	405	410	415
Arg	Arg	His	Leu	Cys	Cys	Gly	Arg	Phe	Arg	Leu	Ala	Asp	Asn	Ser	Asp	420	425	430
Trp	Ser	Lys	Thr	Ala	Thr	Asn	Ile	Ile	Lys	Lys	Ser	Ser	Asp	Asn	Leu	435	440	445
Gly	Lys	Ser	Leu	Ser	Ser	Ser	Ser	Ile	Gly	Ser	Asn	Ser	Thr	Tyr	Leu	450	455	460
Thr	Ser	Lys	Ser	Lys	Ser	Ser	Ser	Thr	Thr	Tyr	Phe	Lys	Arg	Asn	Ser	465	470	475
His	Thr	Asp	Asn	Val	Ser	Tyr	Glu	His	Ser	Phe	Asn	Lys	Ser	Gly	Ser	485	490	495
Leu	Arg	Gln	Cys	Phe	His	Gly	Gln	Val	Leu	Val	Lys	Thr	Gly	Pro	Cys	500	505	510

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<211> 27

<212> DNA

<213> homo sapiens

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Val Gly Pro Gln Arg Lys Thr Leu Val Ser Tyr Val Met Ala Cys Ser
50 55 60
Ile Gly Asn Ile Thr Ile Gln Asn Leu Lys Asp Pro Val Gln Ile Lys
65 70 75 80

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Trp	Asp	Leu	Asn	Lys	Asn	Lys	Ser	Phe	Gly	Gly	Trp	Asn	Thr	Ser	Gly		
			100					105					110				
Cys	Val	Ala	His	Arg	Asp	Ser	Asp	Ala	Ser	Glu	Thr	Val	Cys	Leu	Cys		
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Asn	His	Phe	Thr	His	Phe	Gly	Val	Leu	Met	Asp	Leu	Pro	Arg	Ser	Ala		
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Ser	Gln	Leu	Asp	Ala	Arg	Asn	Thr	Lys	Val	Leu	Thr	Phe	Ile	Ser	Tyr		
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Tyr	Val	Ala	Phe	Glu	Lys	Leu	Arg	Arg	Asp	Tyr	Pro	Ser	Lys	Ile	Leu		
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Met	Asn	Leu	Ser	Thr	Ala	Leu	Leu	Phe	Leu	Asn	Leu	Leu	Phe	Leu	Leu		
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Ala	Val	Leu	Leu	His	Phe	Phe	Leu	Leu	Ala	Thr	Phe	Thr	Trp	Met	Gly		
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Leu	Glu	Ala	Ile	His	Met	Tyr	Ile	Ala	Leu	Val	Lys	Val	Phe	Asn	Thr		
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Tyr	Ile	Arg	Arg	Tyr	Ile	Leu	Lys	Phe	Cys	Ile	Ile	Gly	Trp	Gly	Leu		
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Pro	Ala	Leu	Val	Val	Ser	Val	Val	Leu	Ala	Ser	Arg	Asn	Asn	Asn	Glu		
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Val	Tyr	Gly	Lys	Glu	Ser	Tyr	Gly	Lys	Glu	Lys	Gly	Asp	Glu	Phe	Cys		
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Gln	Ile	Cys	Gly	Arg	Asn	Gly	Lys	Arg	Ser	Asn	Arg	Thr	Leu	Arg	Glu		
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Glu	Val	Leu	Arg	Asn	Leu	Arg	Ser	Val	Val	Ser	Leu	Thr	Phe	Leu	Leu		
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Gly	Met	Thr	Trp	Gly	Phe	Ala	Phe	Phe	Ala	Trp	Gly	Pro	Leu	Asn	Ile		
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Pro	Phe	Met	Tyr	Leu	Phe	Ser	Ile	Phe	Asn	Ser	Leu	Gln	Gly	Lys	Ile		
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<212> DNA

<213> homo sapiens

<400> 33

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 <212> PRT
 <213> homo sapiens

<400> 34

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Asp	Ser	Leu	Ser	Leu	Asp	Asn	Gly	Glu	Ser	Gln	Thr	Lys	Phe	Cys	Gly
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Ala	Thr	Ala	Lys	Gly	Leu	Ser	Phe	Asn	Ser	Ser	Ala	Asn	Glu	Met	His
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Ser	Tyr	Ile	Arg	Val	Ala	Val	Ser	Leu	Arg	Asn	Gln	Lys	Val	Ile	Leu
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Pro	Gln	Thr	Ser	Asp	Ala	Tyr	Gln	Val	Ser	Val	Ala	Lys	Ser	Ile	Ser
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Ile	Pro	Glu	Leu	Ser	Ala	Phe	Thr	Leu	Cys	Phe	Glu	Ala	Thr	Lys	Val
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Gly	His	Glu	Asp	Ser	Asp	Trp	Thr	Ala	Phe	Ser	Tyr	Ser	Asn	Ala	Ser
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Ala	Ser	Cys	Ala	Asp	Leu	Gly	Thr	Leu	Cys	Gln	Asp	Gly	Ile	Ile	Tyr
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Arg	Ile	Ser	Val	Val	Ile	Gln	Asn	Ile	Leu	Arg	His	Pro	Glu	Val	Lys
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Glu	Asp	Lys	Ile	Lys	Val	Lys	Arg	Ser	Leu	Glu	Asp	Glu	Pro	Arg	Leu	435	440	445
Val	Leu	Trp	Ala	Leu	Leu	Val	Tyr	Asn	Ala	Thr	Asn	Asn	Thr	Asn	Leu	450	455	460
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Asp	Glu	Gly	Leu	Arg	Leu	His	Thr	Val	Asn	Val	Arg	Gln	Leu	Gly	His	485	490	495
Cys	Leu	Ala	Met	Glu	Glu	Pro	Lys	Gly	Tyr	Tyr	Trp	Pro	Ser	Ile	Gln	500	505	510
Pro	Ser	Glu	Tyr	Val	Leu	Pro	Cys	Pro	Asp	Lys	Pro	Gly	Phe	Ser	Ala	515	520	525
Ser	Arg	Ile	Cys	Phe	Tyr	Asn	Ala	Thr	Asn	Pro	Leu	Val	Thr	Tyr	Trp	530	535	540
Gly	Pro	Val	Asp	Ile	Ser	Asn	Cys	Leu	Lys	Glu	Ala	Asn	Glu	Val	Ala	545	550	555
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Asn	Ile	Thr	Asn	Ile	Val	Glu	Gln	Val	Lys	Arg	Ile	Val	Asn	Lys	Glu	580	585	590
Glu	Asn	Ile	Asp	Ile	Thr	Leu	Gly	Ser	Thr	Leu	Met	Asn	Ile	Phe	Ser	595	600	605
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 885 890 895
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 Val Leu Ala Ser Arg Asn Asn Asn Glu Val Tyr Gly Lys Glu Ser Tyr
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 Gly Lys Glu Lys Gly Asp Glu Phe Cys Trp Ile Gln Asp Pro Val Ile
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<211> 3582

<212> DNA

<213> homo sapiens

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<400> 36

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Ser	Ala	Val	Trp	Gly	Cys	Ala	Asn	Cys	Arg	Val	Val	Leu	Ser	Asn	Pro
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Ser	Gly	Thr	Phe	Thr	Ser	Pro	Cys	Tyr	Pro	Asn	Asp	Tyr	Pro	Asn	Ser
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Gln	Ala	Cys	Met	Trp	Thr	Leu	Arg	Ala	Pro	Thr	Gly	Tyr	Ile	Ile	Gln
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Ile	Thr	Phe	Asn	Asp	Phe	Asp	Ile	Glu	Glu	Ala	Pro	Asn	Cys	Ile	Tyr
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Asp	Ser	Leu	Ser	Leu	Asp	Asn	Gly	Glu	Ser	Gln	Thr	Lys	Phe	Cys	Gly
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Ala	Thr	Ala	Lys	Gly	Leu	Ser	Phe	Asn	Ser	Ser	Ala	Asn	Glu	Met	His
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Val	Ser	Phe	Ser	Ser	Asp	Phe	Ser	Ile	Gln	Lys	Lys	Gly	Phe	Asn	Ala
	130					135						140			
Ser	Tyr	Ile	Arg	Val	Ala	Val	Ser	Leu	Arg	Asn	Gln	Lys	Val	Ile	Leu
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<211> 690

<212> PRT

<213> homo sapiens

<400> 38

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	595		600		605
Asn Ile Leu Ser Ser Ser Asp Ser Asp Leu Leu Glu Ser Ser Ser Glu					
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Ala Leu Lys Thr Ile Asp Glu Leu Ala Phe Lys Ile Asp Leu Asn Ser					
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Ser Leu Leu Pro Gly Thr Asn Ala Ile Ser Asn Phe Ser Ile Gly Leu					
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<210> 40

<211> 1084

<212> PRT

<213> homo sapiens

<400> 40

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Gln Ala Cys Met Trp Thr Leu Arg Ala Pro Thr Gly Tyr Ile Ile Gln
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Ile Thr Phe Asn Asp Phe Asp Ile Glu Glu Ala Pro Asn Cys Ile Tyr
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Asp Ser Leu Ser Leu Asp Asn Gly Glu Ser Gln Thr Lys Phe Cys Gly
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Ala Thr Ala Lys Gly Leu Ser Phe Asn Ser Ser Ala Asn Glu Met His
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Val Ser Phe Ser Ser Asp Phe Ser Ile Gln Lys Lys Gly Phe Asn Ala
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Ser Tyr Ile Arg Val Ala Val Ser Leu Arg Asn Gln Lys Val Ile Leu
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Pro Gln Thr Ser Asp Ala Tyr Gln Val Ser Val Ala Lys Ser Ile Ser
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Ile Pro Glu Leu Ser Ala Phe Thr Leu Cys Phe Glu Ala Thr Lys Val
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Gly His Glu Asp Ser Asp Trp Thr Ala Phe Ser Tyr Ser Asn Ala Ser
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<213> homo sapiens

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<212> PRT

<213> homo sapiens

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 <212> DNA
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Ser Glu Tyr Val	Leu Pro Cys Pro	Asp Lys Pro	Gly Phe Ser	Ala Ser		
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Arg Ile Cys Phe	Tyr Asn Ala Thr	Asn Pro Leu	Val Thr Tyr	Trp Gly		
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Pro Val Asp Ile	Ser Asn Cys Leu	Lys Glu Ala	Asn Glu Val	Ala Asn		
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Gln Ile Leu Asn	Leu Thr Ala Asp	Gly Gln Asn	Leu Thr Ser	Ala Asn		
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Ile Thr Asn Ile	Val Glu Gln Val	Lys Arg Ile	Val Asn Lys	Glu Glu		
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Asn Ile Asp Ile	Thr Leu Gly Ser	Thr Leu Met	Asn Ile Phe	Ser Asn		
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Leu Lys Thr Ile	Asp Glu Leu Ala	Phe Lys Ile	Asp Leu Asn	Ser Thr		
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 <212> DNA
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<400> 47

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<210> 48

<211> 1083

<212> PRT

<213> homo sapiens

<400> 48

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Gly Thr Phe Thr Ser Pro Cys Tyr Pro Asn Asp Tyr Pro Asn Ser Gln
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Ala Cys Met Trp Thr Leu Arg Ala Pro Thr Gly Tyr Ile Ile Gln Ile
65             70             75             80
Thr Phe Asn Asp Phe Asp Ile Glu Glu Ala Pro Asn Cys Ile Tyr Asp
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Ser Leu Ser Leu Asp Asn Gly Glu Ser Gln Thr Lys Phe Cys Gly Ala
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Val Leu Trp Ala Leu	Leu Val Tyr Asn Ala Thr	Asn Asn Thr Asn Leu
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Glu Gly Lys Ile Ile	Gln Gln Lys Leu Leu Lys	Asn Asn Glu Ser Leu
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Asp Glu Gly Leu Arg	Leu His Thr Val Asn Val	Arg Gln Leu Gly His
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Ser Leu Leu Pro Gly	Thr Asn Ala Ile Ser Asn	Phe Ser Ile Gly Leu
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<212> PRT

<213> homo sapiens

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Sequence Comparison A

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DEFINITION yc50d03.r1 Stratagene liver (#937224) Homo sapiens cDNA clone
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VERSION T71087.1 GI:685608
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SOURCE human.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 520)
AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins
, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore
, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaskis, E.,
Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M.
TITLE Generation and analysis of 280,000 human expressed sequence tags
JOURNAL Genome Res. 6 (9), 807-828 (1996)
MEDLINE 97044478
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
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clone is available royalty-free through LLNL ; contact the IMAGE
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BASE COUNT 138 a 92 c 122 g 162 t 6 others
ORIGIN

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Matches 226; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 62 AAAACAATTGATGAATTGGCCTTCAAGATAGACCTAAATAGCACATCACATGTGAATATT 121

Qy 2023 acaactcggaacttggctctcagcgtatcatccctgttaccaggggacaaatgcaatttca 2082
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DEFINITION  vs94b12.r1 Barstead mouse myotubes MPLRB5 Mus musculus cDNA clone
IMAGE:1153919 5', mRNA sequence
ACCESSION   AA796299
VERSION     AA796299.1  GI:2859254
KEYWORDS    EST.
SOURCE      house mouse.
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            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 472)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K , Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G , Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL    Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:627127
            Seq primer: -28m13 rev2 ET from Amersham.
FEATURES             Location/Qualifiers
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                       /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
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                       TGTTACGAATCTGAAGTGGGAGCGGCCGCCCTTTTTTTTTTTTTTTTTTTT
                       3']; double-stranded cDNA was ligated to Eco RI adaptors
                       [AATTCGGATCCTTG], digested with Not I and cloned into the
                       Not I and Eco RI sites of the modified pT7T3 vector.
                       Library constructed by Bob Barstead. The C2C12 cell line
                       (available from ATCC, catalog # CRL-1772) differentiates
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BASE COUNT      98 a      123 c      111 g      140 t
ORIGIN

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Best Local Similarity 85.7%; Pred. No. 2.5e-78;
Matches 395; Conservative 0; Mismatches 65; Indels 1; Gaps 1;

Qy 2384 ctcaggaagtgcacatcatcccatctgtgaccttctgggatctgaacaaaaacaaaagttttg 2443
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Db 13 CACAGGAAGTCGATCATCTATCTGTGCCTTCTGGGATATGAACAAAAACAAAAGTTTCG 72

Qy 2444 gaggatggaacacgtcaggatgtgttgcacacagagattcagatgcaagtgagacagttct 2503
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 73 GGGGTGGAACAC - TCAGGATGTGTGCCCACTCTGATTGGACGCTGGTGAGACCATT 131

Qy 2504 gcctgtgtaaccacttcacacactttggagttctgatggaccttccaagaagtgcctcac 2563

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Db      132  GTCTGTGAGCCACTTCACTCACTTTGGAGTTCTGATGGATCTTCCAAGGAGTGCCTCAC 191
Qy      2564 agttagatgcaagaaacactaaagtcctcactttcatcagctatatattgggtgtggaatat 2623
Db      192  AAATAGATGGAAGAAACACAAAAGTCCTCACGTTTATTACCTATATTGGGTGCGGAATAT 251
Qy      2624 ctgctattttttcagcagcaactctcctgacatatgttgcttttgagaaattgcaagagg 2683
Db      252  CTGCCATTTTCTCAGCTGCAACTCTCCTGACATATGTTGCTTTTGAGAAGCTGCGCAGGG 311
Qy      2684 attatccctccaaaatcttgatgaacctgagcacagccctgctgttcctgaatctcctct 2743
Db      312  ATTATCCCTCCAAAATCCTGATGAATCTGAGCTCGGCCTTGCTCTTCTGAATCTCATCT 371
Qy      2744 tcctcctagatggctggatcacctccttcaatgtggatggactttgcattgctgttgag 2803
Db      372  TCCTCCTGGATGGCTGGGTCACTTCCTTTGGCGTGGCTGGACTCTGCACGGCTGTGGCTG 431
Qy      2804 tcctgttgcatcttctcctctctggcaacctttacctggatg 2844
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RESULT 8

T71087

LOCUS T71087 520 bp mRNA linear EST 01-MAR-1995
 DEFINITION yc50d03.r1 Stratagene liver (#937224) Homo sapiens cDNA clone
 IMAGE:84101 5', mRNA sequence.

ACCESSION T71087

VERSION T71087.1 GI:685608

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 520)

AUTHORS Hillier,L , Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
 Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins
 ,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore
 ,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,
 Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E.,
 Underwood,K., Wohlmann,P., Waterston,R., Wilson,R. and Marra,M.

TITLE Generation and analysis of 280,000 human expressed sequence tags

JOURNAL Genome Res. 6 (9), 807-828 (1996)

MEDLINE 97044478

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Insert Size: 592

High quality sequence stops: 314 Source IMAGE Consortium, LLNL This
 clone is available royalty-free through LLNL ; contact the IMAGE
 Consortium (info@image.llnl.gov) for further information.

Insert Length: 592 Std Error: 0.00

Seq primer: M13RP1

High quality sequence stop: 314.

FEATURES

source

Location/Qualifiers

1..520

/organism="Homo sapiens"

/db_xref="GDB:501158"

/db_xref="taxon:9606"

/clone="IMAGE:84101"

/clone_lib="Stratagene liver (#937224)"

/sex="male"

/dev_stage="49 years old"

/lab_host="SOLR cells (kanamycin resistant)"

/note="Organ: liver; Vector: pBluescript SK; Site_1: EcoRI"

; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo
dT. Hepatectomy from normal male caucasian. Average insert
size: 1.1 kb; Uni-ZAP XR Vector; -5' adaptor sequence 5'
GAATTCGGCAGG 3' -3' adaptor sequence: 5'
CTCGAGTTTTTTTTTTTTTTTTTTT 3'"

BASE COUNT 138 a 92 c 122 g 162 t 6 others
ORIGIN

Query Match 6.0%; Score 225.4; DB 10; Length 520;
Best Local Similarity 99.6%; Pred. No. 2.8e-47;
Matches 226; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1903 ttttctaataatcttaagcagttcagacagtgacttgcttgagtcattcttgaagcttta 1962
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Db 2 TTTTCTAATATCTTAAGCAGTTCAGACAGTGACTTGCTTGAGTCATCTTCTGAAGCTTTA 61

Qy 1963 aaaacaattgatgaattggccttcaagatagacctaaatagcacatcacatgtgaatatt 2022
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Db 62 AAAACAATTGATGAATTGGCCTTCAAGATAGACCTAAATAGCACATCACATGTGAATATT 121

Qy 2023 acaactcggaacttggctctcagcgtatcatccctgttaccagggacaaatgcaatttca 2082
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Db 122 ACAACTCGGAACCTGGCTCTCAGCGTATCATCCCTGTTACCAGGGACAAATGCAATTTCA 181

Qy 2083 aattttagcattgggtcttccaagcaataatgaatcgattttccagat 2129
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